

A.

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PI Wood WI, Yuan J;

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DR P-PSDB; AAY66757.

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PT Membrane-bound proteins and related nucleotide sequences.

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PS Claim 2; Fig 289; 822pp; English.

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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

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SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 100.0%; Score 570; DB 3; Length 570;

Best Local Similarity 100.0%; Pred. No. 3.9e-89;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy		1 GCGAGGACCGGGTATAAGAAGCCTCGTGCCCTTGCCCCGGGCAGCCGCAGGTTC	60
Db		1 GCGAGGACCGGGTATAAGAAGCCTCGTGCCCTTGCCCCGGGCAGCCGCAGGTTC	60
Qy	61	GCCCCGAGCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTG	120
Db	61	GCCCCGAGCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTG	120
Qy	121	TGCAGCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGT	180
Db	121	TGCAGCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGT	180
Qy	181	GCGCTGGAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTC	240
Db	181	GCGCTGGAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTC	240
Qy	241	AACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGC	300
Db	241	AACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGC	300
Qy	301	TCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAG	360
Db	301	TCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAG	360

Sequence

Comparison

A

[illegible]

Sequence Comparison

RESULT 2

AAY44458

ID AAY44458 standard; protein; 104 AA.

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AC AAY44458;

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DT 27-MAR-2000 (first entry)

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DE Human lung specific gene protein Lng107.

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KW Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;
lung cancer; diagnosis.

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OS Homo sapiens.

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PN WO9960160-A1.

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PD 25-NOV-1999.

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PF 12-MAY-1999; 99WO-US010344.

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PR 21-MAY-1998; 98US-0086212P.

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PA (DIAD-) DIADEXUS LLC.

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PI Yang F, Macina RA, Sun Y;

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DR WPI; 2000-116320/10.

DR N-PSDB; AAZ29723.

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PT A new method for diagnosing, monitoring and staging lung cancer.

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PS Example 2; Page 38-39; 40pp; English.

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CC The present sequence is a lung specific gene (LSG) protein Lng107 from
CC human clone ID 586271. The LSG has high level of tissue specificity for
CC lungs and is overexpressed in cancerous tissues. The sequence serves as a
CC diagnostic marker for detecting, monitoring, staging and prognosticating
CC lung cancer. The diagnosis involves comparing levels of LSG in samples
CC obtained from patient and normal control

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SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 3; Length 104;

Best Local Similarity 100.0%; Pred. No. 1.4e-48;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLAALLGLCVALSCSSAAFLVGS AKPVAQPVAALLESAAEAGAGTLANPLGTLNPLKLL 60

|||||

Db 1 MKLAALLGLCVALSCSSAAFLVGS AKPVAQPVAALLESAAEAGAGTLANPLGTLNPLKLL 60

Qy 61 LSSLGIPVNHLIEGSQKCV AELGPQAVGAVKALKALLGALT VFG 104

|||||

Db 61 LSSLGIPVNHLIEGSQKCV AELGPQAVGAVKALKALLGALT VFG 104



Sequence Comparison 'C'

PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US014484.
 XX
 PR 26-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102686P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgonè GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI; 2000-160673/14.
 DR N-PSDB; AAZ98173.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
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 PS Claim 1; Page 206; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
 CC used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSPP are also used to raise
 CC specific antibodies (Ab) and to screen for agonists and antagonists
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
 CC competitive drug screens, and for purification of HSPP from natural
 CC sources
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 SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 3; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence Comparison

C'

Qy	1	MKLAALLGLCVALSCSSAAAFVLVGS	AKPVAQPVA	ALESAAEAGAGTLANPLGTLNPLKLL	60
Db	1	MKLAALLGLCVALSCSSAAAFVLVGS	AKPVAQPVA	ALESAAEAGAGTLANPLGTLNPLKLL	60
Qy	61	LSSLGIPVNH	LIEGSQKCV	AELGPQAVGAVKALKALLGALT	104
Db	61	LSSLGIPVNH	LIEGSQKCV	AELGPQAVGAVKALKALLGALT	104

